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Molecular serotyping of rough *Salmonella* strains isolated from Danish pork production

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Aim

- To assess the use of molecular serotyping on rough *Salmonella* strains isolated from pig carcasses in Denmark
- To assess if the serotypes obtained by molecular serotyping differed from the serotypes found using traditional serotyping for strains isolated during the same time period from the same source.

Introduction

Surveillance of *Salmonella* in the meat production chain is essential to increase food safety. Serotyping is one of the most commonly used approaches for subtyping *Salmonella*.

Rough strains of S*almonella* autoagglutinate, and this impedes the use of traditional serotyping by agglutination. To overcome this, serotypes can be determined on DNA level, e.g. by using molecular serotyping.

In the present study we used a molecular approach based on the Kauffmann-White scheme to detect the presence of genes encoding the corresponding O and H antigens [1,2]. By using this approach it is possible to compare results with molecular serotyping to results obtained using traditional serotyping.

Materials and Methods

A number of rough *Salmonella* strains (n = 211) isolated from Danish pig carcasses during 2005-2012 were analyzed with molecular serotyping employing Luminex technology (Fig. 1). The assay covers O groups B, C_1, C_2, D, E and O:13, and 33 H antigens [1, 2] . Data from traditional serotyping [3] performed on isolates from the same years (n = 1233) were used for comparison.

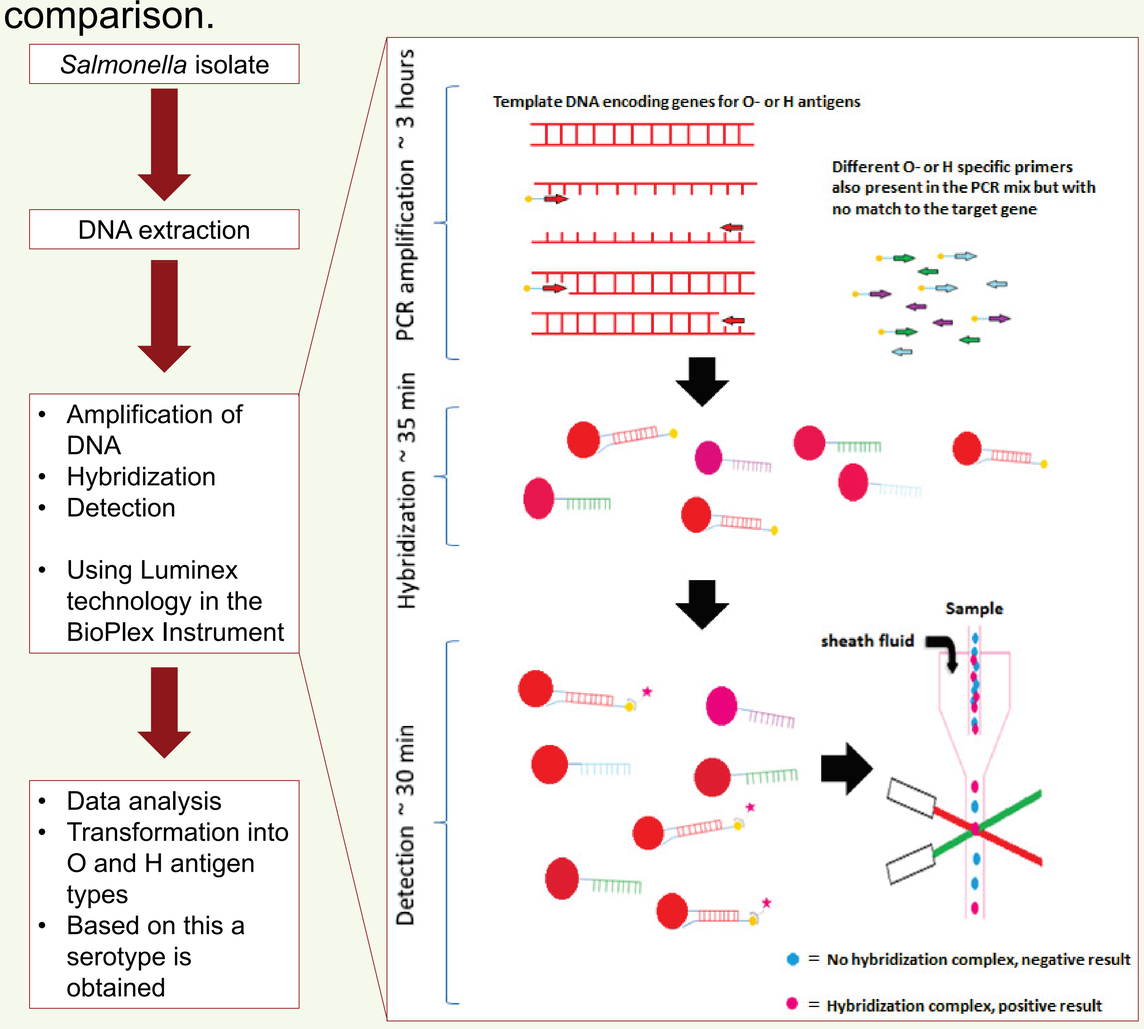


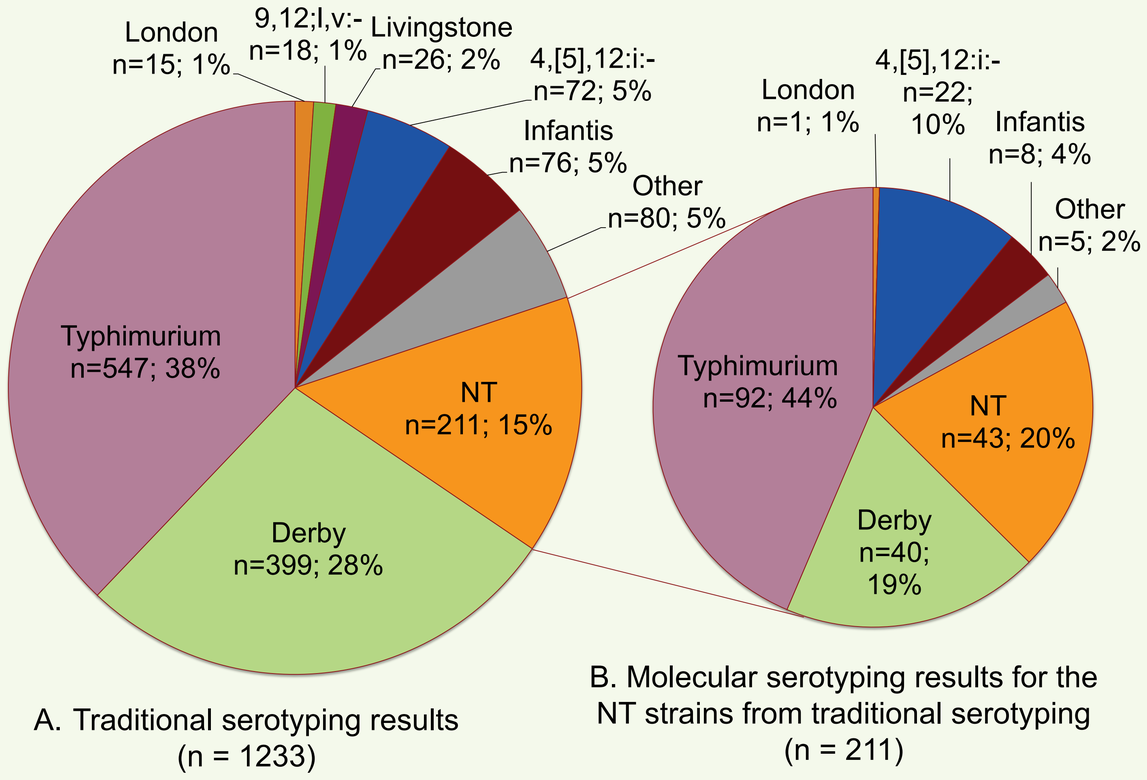
Figure 1. Overview of the molecular serotyping process.

Conclusion

- Serotyping results for molecular serotyping of rough *Salmonella* strains mirrored the serotypes obtained using traditional serotyping for strains isolated from the same source during the same time period.

Results and Discussion

Results show that molecular serotyping enabled serovar identification in 168 of the 211 rough strains (80%) (Fig. 2A & 2B.) Results for strains (n = 1233, Fig. 2A) isolated during the same years from the same source, for which typing using traditional serotyping was possible, showed a similar pattern as the rough strains analyzed using molecular serotyping (Fig. 2B).



A. Traditional serotyping results (n = 1233)

B. Molecular serotyping results for the NT strains from traditional serotyping (n = 211)

Figure 2. Comparison of results obtained for traditional slide agglutination serotyping (diagram A) and molecular serotyping (diagram B). NT: Not typeable (traditional serotyping: rough strains; molecular serotyping: technical problems, or impossible to get complete O and H types). For each serotype the name, no. of strains and % of the total no. of strains are given.

The lack of molecular serotyping results for the 43 strains had several reasons. The most common obstacle was technical issues, that we expect will be solved when re-analyzing the strains.

For about 1/3 of the 43 strains it was not possible to identify the serotype with molecular serotyping, because these types were not covered by the assay. This could be resolved by the inclusion of additional markers.

Studies are in progress to serotype the remaining 43 rough strains using other DNA based techniques (e.g. sequencing) to further assess the difference in results between molecular and traditional serotyping.

References

1. Fitzgerald et. al. 2007 JCM 45 (10): 3323-3334
2. McQuiston et al. 2011 JCM 49 (2): 565-573
3. Grimont, & Weill. 2007. Antigenic Formulae of the Salmonella Serovars, 9th Ed..

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